

SEQUENCE LISTING

<110> ALBANI, SALVATORE

<120> METHOD FOR ISOLATION, QUANTIFICATION, CHARACTERIZATION
AND MODULATION OF ANTIGEN-SPECIFIC T CELLS

<130> AND-TCCCIPI1-DIV1

<140>

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<150> 09/756,983

<151> 2001-01-09

<150> PCT/US99/24666

<151> 1999-10-19

<150> 09/421,506

<151> 1999-10-19

<150> 60/105,018

<151> 1998-10-20

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived
from third hyper V region of IE molecule of Mus musculus

<400> 1

Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys
1 5 10 15

Ala

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived
from bole I protein of Epstein Barr virus

<400> 2

Thr Arg Asp Asp Ala Glu Tyr Leu Leu Gly Arg Glu Ser Val Leu
1 5 10 15

<210> 3
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide derived
 from the haemophilus influenza virus

<400> 3
 Thr Ser Phe Pro Met Arg Gly Asp Leu Ala Lys Arg Glu Pro Asp Lys
 1 5 10 15

<210> 4
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide derived
 from the TCR receptor of Mus musculus

<220>
 <221> MOD_RES
 <222> (18)
 <223> Ser, Ile or Thr

<400> 4
 Leu His Ile Ser Ala Val Asp Pro Glu Asp Ser Ala Val Tyr Phe Cys
 1 5 10 15

Ala Xaa Ser Gln Glu Phe Phe Ser Ser Tyr Glu Gln Tyr Phe Gly Pro
 20 25 30

Gly Thr Arg Leu
 35

<210> 5
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide derived
 from the influenza virus

<400> 5
 Gly Ile Leu Gly Phe Val Phe Thr Leu
 1 5

<210> 6
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived from the influenza virus

<400> 6

Val Lys Leu Gly Glu Phe Tyr Asn Gln
1 5

<210> 7

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (2)

<223> cyclohexylalanine

<400> 7

Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala
1 5 10

<210> 8

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived from the influenza virus

<400> 8

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
1 5 10

<210> 9

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial

<400> 9

Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly
1 5 10 15

Arg

<210> 10
 <211> 15
 <212> PRT
 <213> Escherichia coli

<400> 10
 Gln Lys Arg Ala Ala Tyr Asp Gln Tyr Gly His Ala Ala Phe Glu
 1 5 10 15

<210> 11
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 11
 Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly
 1 5 10 15

<210> 12
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 12
 Gly Ile Leu Gly Phe Val Phe Thr Leu
 1 5

<210> 13
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 13
 Val Lys Leu Gly Glu Phe Tyr Asn Gln
 1 5

<210> 14
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 14
 Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
 1 5 10

<210> 15
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion construct with
 human and bacterial sequences

<220>

<221> CDS

<222> (1)..(939)

<400> 15

atg ggc cac aca cgg agg cag gga aca tca cca tcc aag tgt cca tac	48
Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr	
1 5 10 15	

ctc aat ttc ttt cag ctc ttg gtg ctg gct ggt ctt tct cac ttc tgt	96
Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys	
20 25 30	

tca ggt gtt atc cac gtg acc aag gaa gtg aaa gaa gtg gca acg ctg	144
Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu	
35 40 45	

tcc tgt ggt cac aat gtt tct gtt gaa gag ctg gca caa act cgc atc	192
Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile	
50 55 60	

tac tgg caa aag gag aag aaa atg gtg ctg act atg atg tct ggg gac	240
Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp	
65 70 75 80	

atg aat ata tgg ccc gag tac aag aac cgg acc atc ttt gat atc act	288
Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr	
85 90 95	

aat aac ctc tcc att gtg atc ctg gct ctg cgc cca tct gac gag ggc	336
Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly	
100 105 110	

aca tac gag tgt gtt gtt ctg aag tat gaa aaa gac gct ttc aag cgg	384
Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg	
115 120 125	

gaa cac ctg gct gaa gtg acg tta tca gtc aaa gct gac ttc cct aca	432
Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr	
130 135 140	

cct agt ata tct gac ttt gaa att cca act tct aat att aga agg ata	480
Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile	
145 150 155 160	

att tgc tca acc tct gga ggt ttt cca gag cct cac ctc tcc tgg ttg	528
Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu	
165 170 175	

gaa aat gga gaa gaa tta aat gcc atc aac aca aca gtt tcc caa gat	576
Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp	
180 185 190	

cct gaa act gag ctc tat gct gtt agc gaa ttc ggc ggc tcc ggt ggt	624
Pro Glu Thr Glu Leu Tyr Ala Val Ser Glu Phe Gly Gly Ser Gly Gly	
195 200 205	

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agc gcc aca cct caa aat att act gat ttg tgt gca gaa tac cac aac 672
Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu Tyr His Asn
    210                      215                      220

aca caa ata cat acg cta aat gat aag ata ttt tcg tat aca gaa tct 720
Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr Thr Glu Ser
    225                      230                      235                      240

cta gct gga aaa aga gag atg gct atc att act ttt aag aat ggt gca 768
Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala
    245                      250                      255

act ttt caa gta gaa gta cca ggt agt caa cat ata gat tca caa aaa 816
Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys
    260                      265                      270

aaa gcg att gaa agg atg aag gat acc ctg agg att gca tat ctt act 864
Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala Tyr Leu Thr
    275                      280                      285

gaa gct aaa gtc gaa aag tta tgt gta tgg aat aat aaa acg cct cat 912
Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys Thr Pro His
    290                      295                      300

gcg att gcc gca att agt atg gca aat taa 942
Ala Ile Ala Ala Ile Ser Met Ala Asn
    305                      310

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<210> 16

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<400> 16

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Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 1                      5                      10                      15

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
    20                      25                      30

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
    35                      40                      45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
    50                      55                      60

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
    65                      70                      75                      80

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
    85                      90                      95

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Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
 100 105 110
 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
 115 120 125
 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
 130 135 140
 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
 145 150 155 160
 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
 165 170 175
 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
 180 185 190
 Pro Glu Thr Glu Leu Tyr Ala Val Ser Glu Phe Gly Gly Ser Gly Gly
 195 200 205
 Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu Tyr His Asn
 210 215 220
 Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr Thr Glu Ser
 225 230 235 240
 Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala
 245 250 255
 Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys
 260 265 270
 Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala Tyr Leu Thr
 275 280 285
 Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys Thr Pro His
 290 295 300
 Ala Ile Ala Ala Ile Ser Met Ala Asn
 305 310

<210> 17

<211> 1056

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<220>

<221> CDS

<222> (1)..(1053)

<400> 17

atg gga ctg agt aac att ctc ttt gtg atg gcc ttc ctg ctc tct ggt	48
Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly	
1 5 10 15	
gct gct cct ctg aag att caa gct tat ttc aat gag act gca gac ctg	96
Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu	
20 25 30	
cca tgc caa ttt gca aac tct caa aac caa agc ctg agt gag cta gta	144
Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val	
35 40 45	
gta ttt tgg cag gac cag gaa aac ttg gtt ctg aat gag gta tac tta	192
Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu	
50 55 60	
ggc aaa gag aaa ttt gac agt gtt cat tcc aag tat atg ggc cgc aca	240
Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr	
65 70 75 80	
agt ttt gat tcg gac agt tgg acc ctg aga ctt cac aat ctt cag atc	288
Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile	
85 90 95	
aag gac aag ggc ttg tat caa tgt atc atc cat cac aaa aag ccc aca	336
Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr	
100 105 110	
gga atg att cgc atc cac cag atg aat tct gaa ctg tca gtg ctt gct	384
Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala	
115 120 125	
aac ttc agt caa cct gaa ata gta cca att tct aat ata aca gaa aat	432
Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn	
130 135 140	
gtg tac ata aat ttg acc tgc tca tct ata cac ggt tac cca gaa cct	480
Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro	
145 150 155 160	
aag aag atg agt gtt ttg cta aga acc aag aat tca act atc gag tat	528
Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr	
165 170 175	
gat ggt att atg cag aaa tct caa gat aat gtc aca gaa ctg tac gac	576
Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp	
180 185 190	
gtt tcc atc agc ttg tct gtt tca ttc cct gat gtt acg agc aat atg	624
Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met	
195 200 205	
acc atc ttc tgt att ctg gaa act gac aag acg cgg ctt tta tct tca	672
Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser	
210 215 220	

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cct ttc tct ata gag ctt gag gac cct cag cct ccc cca gac cac gaa 720
Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Glu
225                230                235                240

ttc ggc ggc tcc ggt ggt agc gcc aca cct caa aat att act gat ttg 768
Phe Gly Gly Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu
                245                250                255

tgt gca gaa tac cac aac aca caa ata cat acg cta aat gat aag ata 816
Cys Ala Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile
                260                265                270

ttt tct tat aca gaa tct cta gct gga aaa aga gag atg gct atc att 864
Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile
                275                280                285

act ttt aag aat ggt gca act ttt caa gta gaa gta cca ggt agt caa 912
Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln
                290                295                300

cat ata gat tca caa aaa aaa gcg att gaa agg atg aag gat acc ctg 960
His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu
305                310                315                320

agg att gca tat ctt act gaa gct aaa gtc gaa aag tta tgt gta tgg 1008
Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp
                325                330                335

aat aat aaa acg cct cat gcg att gcc gca att agt atg gca aat taa 1056
Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
                340                345                350

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<210> 18

<211> 351

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<400> 18

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Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly
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Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu
                20                25                30

Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
                35                40                45

Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
50                55                60

Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
65                70                75                80

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Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile
 85 90 95
 Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr
 100 105 110
 Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala
 115 120 125
 Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn
 130 135 140
 Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro
 145 150 155 160
 Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr
 165 170 175
 Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp
 180 185 190
 Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met
 195 200 205
 Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser
 210 215 220
 Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Glu
 225 230 235 240
 Phe Gly Gly Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu
 245 250 255
 Cys Ala Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile
 260 265 270
 Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile
 275 280 285
 Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln
 290 295 300
 His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu
 305 310 315 320
 Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp
 325 330 335
 Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
 340 345 350

<210> 19

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 19

Ser Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala
 1 5 10 15

Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln
 20 25 30

<210> 20

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 20

Ala Gln Leu Lys Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln
 1 5 10 15

Leu Lys Gln Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln
 20 25 30

<210> 21

<211> 1095

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<220>

<221> CDS

<222> (1)..(1092)

<400> 21

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 1 5 10 15

ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc 96
 Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
 20 25 30

atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg 144
 Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
 35 40 45

ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag 192
 Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
 50 55 60

gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag	240
Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu	
65 70 75 80	
gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ctg gaa	288
Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu	
85 90 95	
atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca	336
Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro	
100 105 110	
gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac	384
Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn	
115 120 125	
gtc ctc atc tgt ttc atc gac aag ttc acc cca cca gtg gtc aat gtc	432
Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val	
130 135 140	
acg tgg ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca	480
Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr	
145 150 155 160	
gtc ttc ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc	528
Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu	
165 170 175	
ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac	576
Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His	
180 185 190	
tgg ggc ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca	624
Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro	
195 200 205	
agc cct ctc cca gag act aca gag gaa ttc ggt ggt tcc ggt ggt tcc	672
Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser	
210 215 220	
gcg cag ctg gaa tgg gaa ctg cag gcg ctg gaa aaa gaa aac gcg cag	720
Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln	
225 230 235 240	
ctg gaa tgg gaa ctg cag gcg ctg gaa aaa gaa ctg gcg cag ggc ggc	768
Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly	
245 250 255	
tcc ggt ggt agc gcc aca cct caa aat att act gat ttg tgt gca gaa	816
Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu	
260 265 270	
tac cac aac aca caa ata cat acg cta aat gat aag ata ttt tcg tat	864
Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr	
275 280 285	

aca gaa tct cta gct gga aaa aga gag atg gct atc att act ttt aag 912
 Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys
 290 295 300

aat ggt gca act ttt caa gta gaa gta cca ggt agt caa cat ata gat 960
 Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
 305 310 315 320

tca caa aaa aaa gcg att gaa agg atg aag gat acc ctg agg att gca 1008
 Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala
 325 330 335

tat ctt act gaa gct aaa gtc gaa aag tta tgt gta tgg aat aat aaa 1056
 Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys
 340 345 350

acg cct cat gcg att gcc gca att agt atg gca aat taa 1095
 Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
 355 360

<210> 22

<211> 364

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<400> 22

Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
 1 5 10 15

Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
 20 25 30

Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
 35 40 45

Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
 50 55 60

Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
 65 70 75 80

Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
 85 90 95

Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
 100 105 110

Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
 115 120 125

Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
 130 135 140

Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
 145 150 155 160
 Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
 165 170 175
 Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
 180 185 190
 Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
 195 200 205
 Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser
 210 215 220
 Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln
 225 230 235 240
 Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly
 245 250 255
 Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu
 260 265 270
 Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr
 275 280 285
 Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys
 290 295 300
 Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
 305 310 315 320
 Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala
 325 330 335
 Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys
 340 345 350
 Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
 355 360

<210> 23

<211> 861

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<220>

<221> CDS

<222> (1)..(855)

<400> 23

atg gtg tgt ctg aag ttc cct gga ggc tcc tgc atg gca gct ctg aca	48
Met Val Cys Leu Lys Phe Pro Gly Gly Ser Cys Met Ala Ala Leu Thr	
1 5 10 15	
gtg aca ctg atg gtg ctg agc tcc cca ctg gct ttg gct ggg gac acc	96
Val Thr Leu Met Val Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr	
20 25 30	
cga cca cgt ttc ttg gag cag gtt aaa cat gag tgt cat ttc ttc aac	144
Arg Pro Arg Phe Leu Glu Gln Val Lys His Glu Cys His Phe Phe Asn	
35 40 45	
ggg acg gag cgg gtg cgg ttc ctg gac aga tac ttc tat cac caa gag	192
Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr His Gln Glu	
50 55 60	
gag tac gtg cgc ttc gac agc gac gtg ggg gag tac cgg gcg gtg acg	240
Glu Tyr Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr	
65 70 75 80	
gag ctg ggg cgg cct gat gcc gag tac tgg aac agc cag aag gac ctc	288
Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu	
85 90 95	
ctg gag cag aag cgg gcc gcg gtg gac acc tac tgc aga cac aac tac	336
Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr	
100 105 110	
ggg gtt ggt gag agc ttc aca gtg cag cgg cga gtc tat cct gag gtg	384
Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val	
115 120 125	
act gtg tat cct gca aag acc cag ccc ctg cag cac cac aac ctc ctg	432
Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu	
130 135 140	
gtc tgc tct gtg aat ggt ttc tat cca ggc agc att gaa gtc agg tgg	480
Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp	
145 150 155 160	
ttc cgg aac ggc cag gaa gag aag act ggg gtg gtg tcc aca ggc ctg	528
Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser Thr Gly Leu	
165 170 175	
atc cag aat gga gac tgg acc ttc cag acc ctg gtg atg ctg gaa aca	576
Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr	
180 185 190	
gtt cct cgg agt gga gag gtt tac acc tgc caa gtg gag cac cca agc	624
Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser	
195 200 205	
ctg acg agc cct ctc aca gtg gaa tgg aga gca cgg tct gaa tct gca	672
Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala	
210 215 220	

cag agc aag ggc ggc tcc ggt ggt agc gcc cag ctg aag aag aaa ctc 720
 Gln Ser Lys Gly Gly Ser Gly Gly Ser Ala Gln Leu Lys Lys Lys Leu
 225 230 235 240

cag gct ctg aaa aaa aag aat gcc cag ctc aag cag aag ctg cag gcc 768
 Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala
 245 250 255

ctg aag aaa aag ctg gct cag ggt tcc ggt ggt tcc gcg ggt ggt ggt 816
 Leu Lys Lys Lys Leu Ala Gln Gly Ser Gly Gly Ser Ala Gly Gly Gly
 260 265 270

ttg aac gac atc ttc gaa gct cag aaa atc gaa tgg cac taataa 861
 Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His
 275 280 285

<210> 24

<211> 285

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with
 human and bacterial sequences

<400> 24

Met Val Cys Leu Lys Phe Pro Gly Gly Ser Cys Met Ala Ala Leu Thr
 1 5 10 15

Val Thr Leu Met Val Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr
 20 25 30

Arg Pro Arg Phe Leu Glu Gln Val Lys His Glu Cys His Phe Phe Asn
 35 40 45

Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr His Gln Glu
 50 55 60

Glu Tyr Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr
 65 70 75 80

Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu
 85 90 95

Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr
 100 105 110

Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val
 115 120 125

Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu
 130 135 140

Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp
 145 150 155 160

Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser Thr Gly Leu
 165 170 175

Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr
 180 185 190

Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser
 195 200 205

Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala
 210 215 220

Gln Ser Lys Gly Gly Ser Gly Gly Ser Ala Gln Leu Lys Lys Lys Leu
 225 230 235 240

Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala
 245 250 255

Leu Lys Lys Lys Leu Ala Gln Gly Ser Gly Gly Ser Ala Gly Gly Gly
 260 265 270

Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His
 275 280 285